

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: June 19, 2002, 16:33:07 ; Search time 46.53 Seconds
(Without alignments)
125.761 Million cell updates/sec

Title: US-09-771-961-2
Perfect score: 1709
Sequence: 1 MCSSTGCDLEIRPLDDDLN.....WIOHGWKILGISHEVD 327
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 562222
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_19:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.podent:*
13: sp.yirus:*
14: sp.unclassified:*
15: sp.rvirus:*
16: sp.bacteriap:*
17: sp.archaeap:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1709	100.0	327	4 Q9BZR8	Q9BZR8 homo sapien
2	1189.5	69.6	252	4 Q9BZR7	Q9BZR7 homo sapien
3	1182	69.2	276	4 Q9BZR5	Q9BZR5 mus musculu
4	1082.5	63.3	328	11 Q9CPR0	Q9CPR0 mus musculu
5	1081.5	63.3	328	11 Q9D3W3	Q9D3W3 mus musculu
6	124	7.3	334	4 Q9HB09	Q9HB09 homo sapien
7	121	7.1	250	4 Q96196	Q96196 mus musculu
8	119	7.0	233	11 Q35844	Q35844 mus musculu
9	117	6.8	235	11 Q35843	Q35843 mus musculu
10	116	6.8	188	11 Q9QMX2	Q9QMX2 mus musculu
11	115	6.7	188	4 Q9H1R6	Q9H1R6 mus musculu
12	115	6.7	217	11 Q9N935	Q9N935 mus musculu
13	115	6.7	233	6 Q9N1A2	Q9N1A2 sus scrofa
14	115	6.7	562	10 Q9LX09	Q9LX09 aradidopsis
15	113.5	6.6	386	4 Q9UKN3	Q9UKN3 homo sapien
16	113.5	6.6	1693	3 Q9P655	Q9P655 neurospora

RESULT	1	PRELIMINARY:	PRT:	327 AA.
Q9BZR8	Q9BZR8	Q9BZR8	Q9BZR8	Q9BZR8
AC	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	APOTOMIS REGULATOR BCL-2 LONG FORM.			
GN	BCL2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE-21264734; PubMed-11054413;			
KA	Guo B., Godzik A., Reed J.C.;			
RA	"Bcl-2", a novel pro-apoptotic member of the Bcl-2 family."			
RT	J. Biol. Chem. 276:2780-2785(2001).			
RL	EMBL: AF281254; AAG59793.1;			
DR	InterPro: IPR002475; BCL2_family.			
DR	InterPro: IPR007112; BCL2.			
DR	PIfam: PF00452; BCL2_1.			
DR	SMART: SM00337; BCL2_1.			
DR	PROSITE: PS50062; BCL2_FAMILY.			
DR	PROSITE: PS50062; BCL2_FAMILY.			
SQ	SEQUENCE 327 AA; 36598 MW; 155D43BA01BFB3BA CRC64;			

ALIGNMENTS

Query Match	Similarity	Score	DB 4:	Length 327:
Best local	100.0%	1709	1.1e-129	Indels 0; Gaps 0;
Matches 327:	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	MCSSTGCDLEIRPLDDDLNTEFKILAYTRHHVKSPTALFSPKLLTRSLSGRGLN	60	
DB	1	MCSSTGCDLEIRPLDDDLNTEFKILAYTRHHVKSPTALFSPKLLTRSLSGRGLN	60	
QY	61	CSANSEWTEVSWPCRNSSSEKAINLCKKSSWKAFFGVYEKEDSOSTPAKSAOGRFL	120	
DB	61	CSANSEWTEVSWPCRNSSSEKAINLCKKSSWKAFFGVYEKEDSOSTPAKSAOGRFL	120	

OY 121 EYDSSHQOOWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYMPPOATOGAFKSKKEI 180
 DB 121 EYDSSHQOOWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYMPPOATOGAFKSKKEI 180
 OY 181 FVTEGLSPQLOGHVPVASSSKKDEEQILAKIVELTKYSGDLERKLTCKKAKALMGHPDQ 240
 DB 181 FVTEGLSPQLOGHVPVASSSKKDEEQILAKIVELTKYSGDLERKLTCKKAKALMGHPDQ 240
 OY 241 LSYSEFKITTDQVLMGVDPGSEVKAOGFKAAVLDVYAKLTAIDNHPNRYLGFTKY 300
 DB 241 LSYSEFKITTDQVLMGVDPGSEVKAOGFKAAVLDVYAKLTAIDNHPNRYLGFTKY 300
 OY 301 LKENFSPMIOOHGGMKELTIGSHSEVD 327
 DB 301 LKENFSPMIOOHGGMKELTIGSHSEVD 327

RESULT 2

O9B2R7
 ID 09B2R7 PRELIMINARY: PRT: 252 AA.

01-JUN-2001 (TREMBLrel. 17, Created)
 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 APOPTOSIS REGULATOR BCL-G SHORT FORM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21264734; PubMed=11054413;
 RT "Bcl-G, a novel pro-apoptotic member of the Bcl-2 family."
 RL J. Biol. Chem. 276:2780-2785(2001).
 DR EMBL: AF281255; AAG59794.1;
 SQ SEQUENCE 252 AA; 28089 MW; 87D2E5123EFCB9E4 CRC64;

Query Match
 Best Local Similarity 69.6%; Score 1189.5; DB 4; Length 252;
 Matches 232; Conservative 2; Mismatches 7; Indels 7; Gaps 1;

OY 1 MCTSGCDLEIPDDDDLTETKILAYTRHHVFKSTPALSPKLTSTRSLSGRLGN 60
 DB 1 MCTSGCDLEIPDDDDLTETKILAYTRHHVFKSTPALSPKLTSTRSLSGRLGN 60
 OY 61 CSANESWTEVSWPCRNSSSEKAINLGKKSSKAFEGVEKEDSOSTPAKVSAGQRTL 120
 DB 61 CSANESWTEVSWPCRNSSSEKAINLGKKSSKAFEGVEKEDSOSTPAKVSAGQRTL 120
 OY 121 EYDSSHQOOWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYMPPOATOGAFKSKKEI 180
 DB 121 EYDSSHQOOWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYMPPOATOGAFKSKKEI 180
 OY 181 FVTEGLSPQLOGHVPVASSSKKDEEQILAKIVELTKYSGDLERKLTCKKAKALMGHPDQ 240
 DB 181 FVTEGLSPQLOGHVPVASSSKKDEEQILAKIVELTKYSGDLERKLTCKKAKALMGHPDQ 240
 OY 241 MGHVODGL 241
 DB 241 MGHVODGL 241

RESULT 3
 ID 096OR5 PRELIMINARY: PRT: 276 AA.
 AC 096OR5
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE APOPTOSIS REGULATOR BCL-G MEDIAN FORM.
 GN BCLG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RA Montpetit A., Bolly G., Sinnott D.,
 RT "A detailed transcriptional map of the chromosome 12p12 tumor
 suppressor locus."
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AY040274; AAK72109.1;
 SQ SEQUENCE 276 AA; 30948 MW; 81559A7190F5598E CRC64;

Query Match
 Best Local Similarity 99.1%; Score 1182; DB 4; Length 276;
 Matches 227; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MCTSGCDLEIPDDDDLTETKILAYTRHHVFKSTPALSPKLTSTRSLSGRLGN 60
 DB 1 MCTSGCDLEIPDDDDLTETKILAYTRHHVFKSTPALSPKLTSTRSLSGRLGN 60
 OY 61 CSANESWTEVSWPCRNSSSEKAINLGKKSSKAFEGVEKEDSOSTPAKVSAGQRTL 120
 DB 61 CSANESWTEVSWPCRNSSSEKAINLGKKSSKAFEGVEKEDSOSTPAKVSAGQRTL 120
 OY 121 EYDSSHQOOWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYMPPOATOGAFKSKKEI 180
 DB 121 EYDSSHQOOWSRCLSNVEQCLEHEAVDPKVISIANRVAEIVYMPPOATOGAFKSKKEI 180
 OY 181 FVTEGLSPQLOGHVPVASSSKKDEEQILAKIVELTKYSGDLERKLTCKKAKALMGHPDQ 240
 DB 181 FVTEGLSPQLOGHVPVASSSKKDEEQILAKIVELTKYSGDLERKLTCKKAKALMGHPDQ 240

RESULT 4

O9CPT0
 ID 09CPT0 PRELIMINARY: PRT: 328 AA.

01-JUN-2001 (TREMBLrel. 17, Created)
 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 9030625M01R1K PROTEIN (4933405K19R1K PROTEIN).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=COLON, STOMACH, AND TESTIS;
 RA MEDLINE=21085660; PubMed=11217851;
 RT Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa K., Izawa M., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Saito T., Okazaki Y., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schramm L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Lyons P., Marchionni L., Mashima J., Hume D.A., Kamiya M., Lee N.H.,
 RA Sasaki H., Sato K., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Williams L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,

"Functional annotation of a full-length mouse cDNA collection."

RL Nature 09:685-690(2001). ; -
DR AK018579; BAB31290.1; -
DR EMBL; AK008682; BAB25830.1; -
DR EMBL; AK016570; BAB30370.1; -
DR MGD; MG1:1914063; 9030625M01.Rik.
DR MGD; MG1:1914796; 4933405K19.Rik.
DR InterPro; IPR002475; BCL2_FamIly.
DR InterPro; IPR000572; Euk.oXidored_mol.yb.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS00553; MOLYDOPSTERIN_EUK; UNKNOWN_1.
SQ SEQUENCE 328 AA; 36591 MW; FAC4A7379F008314C CRC64;

Query Match	63.3%;	Score 1082.5;	DB 11;	Length 328;	
Best Local Similarity	67.38;	Pred. No. 3.3e-79;			7.
Matches 224;	Conservative 34;	Mismatches 64;	Indels 11;	Gaps	

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Dh
1 MCSTSVYDIEDIEPIEDDDPDSIEFKALR 118
Oy
61 CSANSEPTWSPGNCNSOSSSEKALINLGKKKSMKAFGVNKEDS -OSTPAKYSAGOR- 118
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
61 WS-TDSMTVOYSLPCGSPSEKSNISLOKCKSSMRLLFVAKKEGGLSPSEKELRAGPQG 119
Dh
119 --TLEYODS-HSOONSRLSNOCLEHEAVDPRVTSIANRVAELVYSMPPOATOQ-GG 174
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
120 PPEVERSGFHNDHMPRISLSTVEORLSESVYDSDKVCINRVAELVYSMPPPDVISHOGG 179
Dh
175 FKSKEIVTEGLSFOLQGHVPAASSCKDEDEPOLIAKIYELLKYSGDOLERKTKKDKALM 214
Oy
180 SKLKE-RVSEILYFEREG--PDCSKNKDGDQJLISYVELKLFSDOLGRIKDKKALM 235
Dh
235 GHFOGLSVEYKTIIDVOYLMGVDPGRSEVSEYKAGOFKAAIYIVTAKTLAIDHNPANVL 294
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
236 SSFODLSYFKITDOLFRLVDVDTGSESEVAKRFAKALAIADIAIKTLAIDHNPANML 295
Oy
295 GFCTKYLKENSPYAOOHGGMEKILGISHEEVD 327
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
296 GFCTKYLREYFSPWVOONGHGEKILGISHEEVD 328
Dh

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RESULT      5
09D3M3
ID          09D3M3
AC          09D3M3
01-JUN-2001 (TREMBlrel. 17, Created)
01-JUN-2001 (TREMBlrel. 17, Last sequence update)
01-JUN-2001 (TREMBlrel. 17, Last annotation update)
4933405K19RIK
4933405K19RIK
DE          Mus musculus (mouse).
CN          Mus musculus (mouse).
OS          Mus musculus (mouse).
CS          Mus musculus (mouse).
CC          Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_taxid-10090;
[1]
SEQUENCE FROM N.A.
STRIN=NC57BL/6J; TISSUE=TESTIS;
MEDLINE=21085660; PubMed=11217851;
Kawai T., Shlnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Akaichi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gotohori T., Bono H., Kankawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Rietschmann W., Gaasterland T., Gissi C., Kling B., Kochiya H.,
Fleischmann W., Gaasterland T., Gissi C., Kling B., Kochiya H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schirral L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Bash G.,
Blake J., Boffelli D., Boujunga N., Carlini P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

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RA Sasaki H., Sato K., Schoenbach C., Seya T., Shiba Y., Storch K.-F.,
RA Suzuki H., Togo-Oka K., Wang K. H., Wetz C., Whittaker C., Wilming L.,
RA Ynusha-Boris A., Ioshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RL EMBL: AK016897; BMB3340581981.
DR EMBL: AK016897; BMB3340581981.
DR MGI: MGI:1914796; B2C2 family.
DR InterPro: IPR002475; B2C2 family.
DR PROSITE: PS50062; B2C2 FAMILY: 1.
SQ SEQUENCE 328 AA: 37036 FM: 7919C5A441C62C4 CRC64;

Query Match	63.38;	Score 1081.5;	DB 11;	Length 328;	
Best Local Similarity	67.38;	Pred. No. 3.9e-79;			7
Matches 224;	Conservative 34;	Mismatches 64;	Indels 11;	Gaps	

[illegible]

RESULT	6	PRELIMINARY:	PRT:	334 AA.
ID	09HB09			
AC	09HB09;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, last sentence update)			
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DE	BCL-2 RELATED PROLINE-RICH PROTEIN.			
GN	BCL2L12.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Eukaryota; Metazoa; Primates; Catarrhini; Hominoidea; Homo.			
OC	Mammalia;			
OX	NCBI_TaxID=9606;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RA	MEDLINE=21295042; Pubmed=11401436;			
RA	Scorlles A., Kyriakopoulos L., Yousef G.M., Ashworth L.K., Kwame A.,			
RA	Diamandis E.P.;			
RT	"Molecular cloning, physical mapping, and expression analysis of a			
RT	novel gene, BCL2L12, encoding a proline-rich protein with a highly			
RT	conserved BH2 domain of the Bcl-2 family.";			
RT	Genomics 72:217-221(1995). "			
RL	EMBL: AF289220; AAG29495.1.			
DR	EMBL: AF289220; AAG29495.1; 539854C83E7CAB7 CRC64;			
DR	SEQUENCE 334 AA; 36821 MW;			
SO				

Query Match 7.3%; Score 12.7; Indels 58; Gaps 13;
Best Local Similarity 22.9%; Pred. No. 0.053;
Matches 65; Conservative 43; Mismatches 118;
WTEVSM---PCRNSSSEKALNLGKKKSSKAFEGVEKEKDSQTPAKVSAQGORTLEFY 123

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Db 72 WRRRRGPGPGAGMAGSEEE---LGREDTFLVLAALRGEAGSPVPPSPPAQDEPT 128
QY 124 DSHSQOQMSRCLSNVEOCL-----EHEAVDPKVISIANRVAEIIYSSWPPPOAT---QAG 173
Db 129 D-----FLSRRLRCLEPCSLGRGAAPSESPRCSLPDIRC---YGLEPAPAPDFYAL 177
QY 174 GPKSEIYVTEGL-----SFOLOGHVPVASSSKKDEEOQLAKIYVELLYKSGDOLERKLR 229
Db 178 VAQRLEQVQEQOLKSPSPPEILOG-----PPSTEKEAILRLVALLLEEAIVINQKRLAS 230
QY 230 DKALMGHPDGLSYSVFRTINDVLAQV-----PRESEVKAQGFALVIDY 278
Db 231 DPALRSKLY-RLSDFARLVELFCSSRDSSRPSRACPGPPSPPEPLA---RLALAMEL 286
QY 279 TAKTLAIDNHPMRVYGFGRYIKENFSPWIOOHGMEKILGIS 322
Db 287 SRRVAGIG-----GTLAGLSVEHV-HSFTPMIAHGMEGILAVS 241

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RESULT 7
AC 096196 PRELIMINARY; PRT; 250 AA.
DT 01-DEC-2001 (TREMBlrel, 19, Created)
DT 01-DEC-2001 (TREMBlrel, 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel, 19, Last sequence update)
DE SIMILAR TO RIKEN CDNA 5430429M05 GENE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN NCBI_Taxid=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS; AND LEIOMYOSARCOMA;
RA Straussberg R.;
DR Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007724; AAH07724.1;
SQ SEQUENCE 250 AA; 26897 MW; 619B6F7DBF73664 CRC64;

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Query Match
Best Local Similarity 7.1%; Score 121; DB 4; Length 250;
Matches 68; Conservative 44; Mismatches 102; Indels 122; Gaps 14;
QY 10 EELPDDDDINTIEFKILAYTRHHFKSTPALFSRK-----LLTRSLSORGLG 59
Db 5 EELGLREDTL-----RVLAFLRGEAGSPVPTPRSPAOEPTDLRLRCLPCSLG 59
QY 60 NCSEA-NESWTEVSMPCRNSSQSEKAINLGKKSSWKAFFGVVEKEDSOTPAKVSAGOR 118
Db 60 RGAAPSESPRCSLPDIR-----PCYGL---EPGPAPPDFFALVAQR 97
QY 119 TLEYGDSHQSOMSRCLSNVEOCLHEAVDPKVISIANRVAEIIYSSWPPPOATQAGFKSR 178
Db 98 -----LEQLVQEQOLKSP-----PSP----- 112
QY 179 EIVTEGLSFOLOGHVPVASSSKKDEEOQLAKIYVELLYKSGDOLERKLRKKKALMGHQ 238
Db 113 -----ELLOG-----PPSTEKEAILRLVALLLEEAIVINQKRLAS 230
QY 239 DGLSYSVFRTINDVLAQV-----PRESEVKAQGFALVIDY 278
Db 156 -RLSDFARLVELFCSSRDSSRPSRACPGPPSPPEPLA---RLALAMEL 286
QY 287 NHPMRVYGFGRYIKENFSPWIOOHGMEKILGIS 322
Db 211 -----GTLAGLSVEHV-HSFTPMIAHGMEGILAVS 241

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RESULT 8
ID 035844 PRELIMINARY; PRT; 233 AA.

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AC 035844;
DT 01-JAN-1998 (TREMBlrel, 05, Created)
DT 01-JAN-1998 (TREMBlrel, 05, Last sequence update)
DE 01-DEC-2001 (TREMBlrel, 19, Last sequence update)
DE BCL-XL.
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_Taxid=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=B6/CBA; TISSUE=THYMUS;
RA MEDLINE=96051053; PubMed=9390687;
RX Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-2 isoform connected to the T cell receptor regulates
RT apoptosis in T cells."
RL Immunity 7:629-639(1997).
DR HSP; U51278; AAC53459.1;
DR HSP; P53563; IAF3.
DR MGD; MGI:88139; Bcl2L.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl_2.
DR Pfam: PF00452; Bcl-2; 1.
DR Pfam: PF02180; B4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; B4; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS0063; BH4-2; 1.
SQ SEQUENCE 233 AA; 26033 MW; 3083P2D8327E072E CRC64;

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Query Match
Best Local Similarity 7.0%; Score 119; DB 11; Length 233;
Matches 54; Conservative 37; Mismatches 91; Indels 74; Gaps 11;
QY 77 SOSSEKAI-----NLGKKSSWKAFFGVVEKEDSOTPAKVSAGORLEQDSHQSOM 130
Db 2 SOSRELVDLFLSYKLSQGYSSWSQSFSDVEENR-----TEAPETAEETPSAINGNSW 57
QY 131 SRCLSNVEOCLHEAVDPKVISIANRVAEIIYSSWPPPOATQAGFKSRKEIVTEGLSFO 190
Db 58 -----HLADSPAY-----NGAT----- 69
QY 191 OGHVPVASSSKKDEEOQLAKIYVELLYKSGDOLERKLRKKKALMGHPDGLSYSVF 246
Db 70 -GH-----SSSLDAREVIMPAVAQALREAGDEFEELRYRRAFSDLTSLHTTPGTAQOSF 123
QY 247 KTTIDVLAQV-----GVDPGRSEVKAQGFALVIDY 278
Db 124 EOYVNEELFRGVN---WGRIVAFPSFGALCVESVDKEMV---LVSRLASWATYLNHDL 178
QY 306 SPTIOOHGMEKILGI 321
Db 179 EPWIOHNGMDTFVDL 194

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RESULT 9
ID 035843 PRELIMINARY; PRT; 235 AA.
DT 01-JAN-1998 (TREMBlrel, 05, Created)
DT 01-JAN-1998 (TREMBlrel, 05, Last sequence update)
DE 01-DEC-2001 (TREMBlrel, 19, Last sequence update)
DE BCL-X-GAMMA.
GN BCL2L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. TISSUE=THYMUS;
RC STRAIN=B6/CBA; PubMed=9390687;
RX MEDLINE=98051053; PubMed=9390687;
RA Yang X.-F., Weber G.F., Cantor H.;
RT "A novel Bcl-x isoform connected to the T cell receptor regulates
apoptosis in T cells."
RL Immunity 7:629-639(1997);
EMBL: U51277; AAC53458.1; -
DR HSSP; P53563; Bcl2L1.
DR MGD; MGI:88139; Bcl2L1.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; BCL_2.
DR InterPro; IPR003093; BH4.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS01260; BH4_2; 1.
DR PROSITE; PS00663; BH4_2; 1.
SO SEQUENCE 235 AA; 26122 MW; 649D914C2D5378F6 CRC64;
Query Match 6.8%; Score 117; DB 11; Length 235;
Best Local Similarity 21.8%; Pred. No. 0.12; 88; Indels 78; Gaps 12;
Matches 56; Conservative 35; Mismatches 130
OY 77 SOSSEKAI-----NLGKKSSWKAFPGVVEKEDSOSTPAKVSAGQRTLEYQDSHSQOW 130
DB 2 SOSNRELIVDFLSYKLSQGYMSQFSDVEENR-----TEAPEETEARETPSAINGNPSW 57
DB 131 SRCLSNVEQCLEHEAVDPKVISIANRVAEIYSWPPQATQAGGFKSEIFVTBGLSFOL 190
OY 58 -----HLADSPAV-----NGAT----- 69
DB 191 OGHPVASSSSKKDEEPI-LAKIVELKYSQDLE---RLKKDKALMGHPDGLSYSVF 246
OY 70 -GH-----SSLDAREVIMAAVKQALREAGDEFLRTYRAFSDLTSQLHTPTGAYOSF 123
DB 247 KITTDQVLM-GVDPGRSESEVKAQGEKALVDTAKLTALDHPNPNRVLGCTGYLKENE 305
OY 124 EQVNELEFRDGVN--WGRIVAFSFGALCVESVDKEMQV---LVSRIASMMATYIINDHL 178
DB 306 SPWIOOHGGMKILGIS 322
OY 179 EFWIDENGW-----GVS 191
RESULT 10
OQ9MX2 PRELIMINARY: PRT; 188 AA.
AC 090MX2: (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 19, Last annotation update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BCL-X (FRAGMENT).
GN BCL2L1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20350651; PubMed=10894153;
RX Rucker E.B. III, Dierissen P., Wagner K.U., Garrett L.,
RA Wynshaw-Boris A., Flaws J.A., Hennighausen L.;
RT "Bcl-x and Bax regulate mouse primordial germ cell survival and
apoptosis during embryogenesis.";

RL Mol. Endocrinol. 14:1038-1052(2000).
DR EMBL; AF088904; AAC72232.1; -
DR HSSP; P53563; IAF3.
DR MGD; MGI:88139; Bcl2L1.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; BCL_2.
DR InterPro; IPR003093; BH4.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS01260; BH4_2; 1.
DR PROSITE; PS00663; BH4_2; 1.
FT NON TER 188 188
SO SEQUENCE 188 AA; 21126 MW; 4E62F8356D248E52 CRC64;
Query Match 6.8%; Score 116; DB 11; Length 188;
Best Local Similarity 21.6%; Pred. No. 0.11; 88; Indels 74; Gaps 11;
Matches 54; Conservative 34; Mismatches 130
OY 77 SOSSEKAI-----NLGKKSSWKAFPGVVEKEDSOSTPAKVSAGQRTLEYQDSHSQOW 130
DB 2 SOSNRELIVDFLSYKLSQGYMSQFSDVEENR-----TEAPEETEARETPSAINGNPSW 57
DB 131 SRCLSNVEQCLEHEAVDPKVISIANRVAEIYSWPPQATQAGGFKSEIFVTBGLSFOL 190
OY 58 -----HLADSPAV-----NGAT----- 69
DB 191 OGHPVASSSSKKDEEPI-LAKIVELKYSQDLE---RLKKDKALMGHPDGLSYSVF 246
OY 70 -GH-----SSLDAREVIMAAVKQALREAGDEFLRTYRAFSDLTSQLHTPTGAYOSF 123
DB 247 KITTDQVLM-GVDPGRSESEVKAQGEKALVDTAKLTALDHPNPNRVLGCTGYLKENE 305
OY 124 EQVNELEFRDGVN--WGRIVAFSFGALCVESVDKEMQV---LVSRIASMMATYIINDHL 178
DB 306 SPWIOOHGGM 315
OY 179 EFWIDENGW 188
RESULT 11
OQ9H1R6 PRELIMINARY: PRT; 188 AA.
AC 09H1R6: (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 19, Last annotation update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BA243J16.1.1 (BCL2-LIKE 1 (ISOFORM 1)) (FRAGMENT).
GN BCL2L1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Brown A.; (MAY-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL160175; CAC10003.1; -
DR HSSP; Q07817; ILYX.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR000712; BCL_2.
DR InterPro; IPR003093; BH4.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.

DR PROSITE: PS50063; BH4-2; 1.
FT NON_TER 188 188
SQ SEQUENCE 188 AA; 21029 MW; 7074B6095145C324 CRC64;

Query Match
Best Local Similarity 6.7%; Score 115; DB 4; Length 188;
Matches 54; Conservative 34; Mismatches 80; Indels 90; Gaps 12;

QY 77 SOSSEKAI-----NLGKKSSMKAFPGVVEK-----EDSOSTPAKVSAGQRTLEY 122
DB 2 SOSNRELVDLSYKLSQKGYSMGFSVEENKTEAEGETSEMEPEPSALNG-----53
QY 123 QDSHQQMSRCLSNVEQCLEHAEDPVYISIANRVAEIVSWPPQATQAGGKKEIEV 182
DB 54 ----NPSW-----HLADSPAV-----65
QY 183 TEGSLFQLOGHVPAVASSKKDEEQI-LAKIVLELYSGDLE--RKLKKDALKMGHPQ 238
DB 66 -NGAT-----GH-----SSSIDAREVIMPAVAKQALREAGDEFEELRYRRAFSDLTSQLHIT 115
DB 239 DGLSYVEFTITDOVLM-GVDPGSESEVKAQGFKAALVIDYAKLTALIDNHPNRYLGEF 297
QY 116 PGTAQOSFOVNELEFRDGVN--WGRIVAFSFGALCVESVDKEMQV--LVSRIAMM 170
DB 298 TTYLKENFSPMIOHGM 315
DB 171 ATYLDHLEPMIOWENGW 188

RESULT 12

ID 099N35 PRELIMINARY; PRT; 217 AA.
AC 099N35;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE B-CELL LEUKEMIA/LYMPHOMA 19, last annotation update)
GN BCLX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Tang X.-F., Cantor H.;
RT "Novel cDNA structure and genomic organization of apoptosis regulatory
gene Bcl-x-gamma." to the EMBL/GenBank/DBJ databases.
FI EMBL: AF133282; AKR15455.1;
LA EMBL: AF133281; AKR15455.1; JOINED.
DR HSP: P53563; IAF3.
DR InterPro: IPR002475; BCL2 family.
DR InterPro: IPR000712; BCL-2.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL2.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
FT NON_TER 1
SQ SEQUENCE 217 AA; 24234 MW; 3B5A4E809A7DEF18 CRC64;

Query Match
Best Local Similarity 6.7%; Score 115; DB 11; Length 217;
Matches 51; Conservative 34; Mismatches 88; Indels 68; Gaps 10;

QY 86 LGKSSMKAFPGVVEKEDSOSTPAKVSAGQRTLEYDSSHQMSRCLSNVEQCLEHEA 145
DB 1 LSGKGSMSQSFSDVEENR-----TEAPEETEARETRPPSALNGNPSW-----HLA 44

QY 146 VDPKVISIANRVAEIVSWPPQATQAGGKKEIEFTGSLFQLOGHVPAVASSKKDEE 205
DB 45 DSPAV-----NGAT-----SSSIDAR 62
QY 206 EOI-LAKIVLELYSGDLE--RKLKKDALKMGHPQDGLSYVEFTITDOVLM-GVDP 260
DB 63 EYIPMAVAKQALREAGDEFEELRYRRAFSDLTSQLHITPGTAQOSFEQVNELEFRDGVN--120
QY 261 GESEVKAQGFKAALVIDYAKLTALIDNHPNRYLGEFTKYLENFSPIQOHGGMKEIK 320
DB 121 WGRIVAFSFGALCVESVDKEMQV--LVSRIAMMAYTLNDHLEPMIOWENGWDTFVD 177
QY 321 I 321
DB 178 L 178

RESULT 13

ID 09N1A2 PRELIMINARY; PRT; 233 AA.
AC 09N1A2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE ANTI-APOPTOTIC REGULATOR BCL-XL.
GN BCL-XL.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Lee T.L., Canty J.M.;
RT "PCR Cloning of a porcine bcl-xL cDNA from Heart."
FI Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
LA EMBL: AF216205; AAF33212.1;
DR HSP: 007617; IMAZ.
DR InterPro: IPR002475; BCL2 family.
DR InterPro: IPR000712; BCL-2.
DR Pfam: PF00452; BCL-2; 1.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL2.
DR SMART: SM00337; BCL2.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS01260; BH4; 1.
DR PROSITE: PS50063; BH4-2; 1.
SQ SEQUENCE 233 AA; 26047 MW; 2FA312819B25E17D CRC64;

Query Match
Best Local Similarity 6.7%; Score 115; DB 6; Length 233;
Matches 54; Conservative 34; Mismatches 89; Indels 74; Gaps 11;

QY 77 SOSSEKAI-----NLGKKSSMKAFPGVVEKEDSOSTPAKVSAGQRTLEYDSSHQGM 130
DB 2 SOSNRELVDLSYKLSQKGYSMGFSVEENKTEAEGETSEMEPEPSALNG-----34
QY 131 SRCLSNVEQCLEHAEDPVYISIANRVAEIVSWPPQATQAGGKKEIEFTGSLFQ 190
DB 35 -----TEAPEETEARETRPPSALNGNPSW-----SWHLADSPAVNG-----A 68
QY 191 OGHVPAVASSKKDEEQI-LAKIVLELYSGDLE--RKLKKDALKMGHPQDGLSYVE 246
DB 69 TGH-----SSSIDAREVIMPAVAKQALREAGDEFEELRYRRAFSDLTSQLHITPGTAQSF 123
QY 247 KITTDQVLM-GVDPGSESEVKAQGFKAALVIDYAKLTALIDNHPNRYLGEFTKYLEN 305
DB 124 EQVNELEFRDGVN--WGRIVAFSFGALCVESVDKEMQV--LVSRIAMMAYTLNDH 178

OY 306 SPWIOHGWE 316
 DB 179 EPWIOGSGMD 189

RESULT 14

O9LXU9

PRELIMINARY; PRT; 562 AA.

ID O9LXU9

AC O9LXU9; PRELIMINARY; PRT; 562 AA.

DT 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DE HYPOHETICAL 63.3 KDA PROTEIN.

GN 724H18.70.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.

NCBI_TaxID=3702;

RN (1)

RP SEQUENCE FROM N.A.

RA Bevan M., Robben J., Grymonprez B., Volckaert G., Bancroft I.,

RA Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RN (2)

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL253013; CAB88254.1; -.

KW Hypothetical protein.

SQ SEQUENCE 562 AA; 63328 MW; CFB25EC6ED529F0 CRC64;

Query Match 6.7%; Score 115; DB 10; Length 562;

Best Local Similarity 21.7%; Pred. No. 0.58; Indels 110; Gaps 16;

Matches 80; Conservative 43; Mismatches 136; Indels 110; Gaps 16;

OY 31 TRHVFSTPALFSPKL-----LRTSL-----ORGLGNCANESWTEVS 71

DB 128 SHHIVYMSDALRSPPLHFTYTGSRNCGSVDFRSVSSCNDYKOKGFDKSLKSNLVY- 186

OY 72 WPCRNSSG---SEKAINIG-----KKSSWKAFF---GYVEKDSOSTPAKVSA 114

DB 187 -PLTDSHSAVVSQPRNNGGRVSWLFPKLLKKOKSNSIFNSPSITEKSEVSEVVKDSG 245

OY 115 QGGRTLEQ-----DSHSGQMSRCLSNVPCLEH---EAVDPKVISIANRVAEIVY 162

DB 246 SGVEKLKRLMEANRSDAALTOVSEKSSIGLESEKLOYLESYCDNLKALREATEVY- 304

OY 163 SWPPQATQAG---GFKSEIFVTEGLSFOLOGHVPVASS-----SKRDEE 206

DB 305 ---SQENSGRSSGKKNSEMPVSE--EYVMEGFLQIVSEARLSIKOFLTLVSEIDEED 358

OY 207 QILAKIVELLKYSGLERKLLKKDALKMGHPQDGLSYVFKITTDYVLMG-----VDPK 260

DB 359 STLGINITL-LQPHNLFTSKYSKIIQYHLALIISSQSVYODFENCVFQKNGKPKLLDPE 417

OY 261 GESEYKAGFAALIVDTAKLIDNHPMNRVLGFTKYLENFS----- 306

DB 418 QDRONNESSF-----ASLRNLSMNEVLKGTIKYSDPSRFDCKMSLIITTL 465

OY 307 ---PWIOQ 311

DB 466 NWTTPWSEQ 474

RESULT 15

O9UKN3

PRELIMINARY; PRT; 386 AA.

AC O9UKN3

DT 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE MILI PROTEIN.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

OX (1)

RP SEQUENCE FROM N.A.

RA Zemskova M.Y., Lilly M., Escher A.P.;

RT "Mili, a novel human gene encoding mitochondria located protein

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF146568; AAF03602.1; -.

DR InterPro: IPR002475; BCL2_family.

DR Pfam: PF00452; Bcl-2; 1.

DR SMART: SM00337; BCL; 1.

DR PROSITE: P55062; BCL2_FAMILY; 1.

SQ SEQUENCE 386 AA; 41726 MW; B8F2B17507D81BC7 CRC64;

Query Match 6.6%; Score 113.5; DB 4; Length 386;

Best Local Similarity 26.1%; Pred. No. 0.46; Indels 17; Gaps 3;

Matches 31; Conservative 25; Mismatches 46; Indels 17; Gaps 3;

OY 214 ELKYSGLERKLLK--DKALMGHPQDGLSYVFKITTDYVLMGVDPRGESEYKAGFK 271

DB 3 DCLAHGEEKYSOELEKEPLKHALQMLISQPVYQAFRECT-----LETTVASGWN 52

OY 272 AALV-----IDVTKALAIQNHPMNRVYLGFTKYLENFSWIOHGMEKILGISHEE 325

DB 53 KILVPLVLLKQMLLETRLGOEPLSALLQFGVYTLIEDYSAEYIIQGGMGVYFSLESE 111

Search completed: June 19, 2002, 16:39:44

Job time: 397 sec

